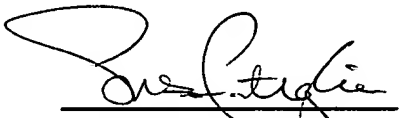
the four sequences shown in Figure 2(C) into the description of that figure at specification page 5. Attached hereto is a page entitled "Version With Markings to Show Changes Made". It is respectfully submitted that no new matter has been introduced.

An early and favorable action on the merits is earnestly sought.

Respectfully submitted,



Susan Petraglia
Reg. No. 35,044

Attachment: 1 page entitled "Version with markings to show changes made"

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Appl. No. 09/603,885

Version with Markings to Show Changes Made

In the specification:

Paragraph beginning with "Figure 2:" on page 5 and continuing to page 6 has been amended as follows:

Figure 2: (A) Schematic representation of a leucine zipper pair visualized from the *N*-terminus illustrating e/g-interactions and the hydrophobic core formed by the a- and d-positions. (B) Distribution of residues at the semi-randomized positions throughout selection. The number of zipper pairs sequenced is given in parentheses, save "Before selection" where the theoretical distribution is reported. Each pair carries one core a-pair and 6 e/g-pairs. Neutral e/g-pairs have one or both residues as Gln. In "Competition (I114A)" only clones from P6 to P12 (not from earlier passages) were considered for analysis. Thus, 37 individual clones were identified, giving rise to 10 unique sequences due to multiple [occurrence] occurrence of the enriched clones. The distributions were calculated according to the frequency of sequence [occurrence] occurrence (n=37). (C) Leucine zipper sequences WinZip-A1 (SEQ ID NO:1), WinZip-B1 (SEQ ID NO:2), WinZip-A2 (SEQ ID NO:3) and WinZip-B2 (SEQ ID NO:4) obtained after competition selection and chain shuffling. The heptad positions (*a* to *g*) are followed by the heptad number (1 to 5). Invariant residues from GCN4 are underlined. Clear boxes indicate the semi-randomized e- and g-positions (black outline) and core a-position (a3) (grey outline). Circled residues were designed to contribute to helix capping. Shaded residues were designed for the introduction of restriction sites. Other residues are from c-Jun (LibA) or c-Fos (LibB). Arrows indicate putative e/g-interactions.